CX7-131WO2_ST25

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<110> Codexis, Inc.
Huisman, Gjalt W.
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Mijts, Benjamin
Vroom, Jonathan
Zhang, Xiyun

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atgtttggtg ttcaggcagt tgatctgcgt acctacaaaa aaaccggtca ttatgatgca 1500

cgtgcctgtc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

cagtatccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgtgtctgca t 1701

<210> 6
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 6

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Leu Thr Ile Asn Asp Val Val Arg Val Ala Arg Asn Gly Thr Leu Val
35 40 45

Ser Leu Thr Asn Asn Thr Asp Ile Leu Gln Gly Ile Gln Ala Ser Cys
50 55 60

Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val
65 70 75 80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
85 90 95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
100 105 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg

115 120 125

Ala Asn Ser His Met Arg Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
130 135 140

Lys Arg Met Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145 150 155 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
165 170 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
180 185 190

Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
195 200 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
210 215 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225 230 235 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Gly
245 250 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
260 265 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
275 280 285

Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
290 295 300

Arg Asp His Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro

305 310 315 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
325 330 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
340 345 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
355 360 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Leu Leu Ala Lys
370 375 380

His Leu Asp Val Gln Ile Ala Leu Leu Val Ser Pro Glu Phe Asn Asn
385 390 395 400

Gly Leu Pro Ala Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
405 410 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
420 425 430

Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
435 440 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
450 455 460

Ala Arg Arg Ser Val Asp Ile Phe Gln Asn Tyr Val Ala Ile Ala Leu
465 470 475 480

Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
485 490 495

His Tyr Asp Ala Arg Ala Cys Leu Ser Pro Ala Thr Glu Arg Leu Tyr

500 505 510

Ser Ala Val Arg His Val Val Gly Gln Tyr Pro Ser Ser Asp Arg Pro
515 520 525

Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
530 535 540

Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545 550 555 560

Asp Ile Leu Pro Cys Leu His
565

<210> 7
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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caggccagct gtgattatat caataatgca gttgaaagcg gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gcaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc gtggtgcaag cggtattcgt 420

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gaatttggta gcattggtgc cagcggtgat ctggttccgc tgagctatat taccggtagc 540

ctgattggcc tggacccgag ctttaaagtt gattttaatg gcaaagaaat ggacgcaccg 600

accgcactgc gtcagctgaa tctgagtccg ctgaccctgc tgccgaaaga aggtctggca 660

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ggtctgcctc cgagtctgct gggtaatcgt gaacgtaaag ttaatatggg tctgaaaggt 1260

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agcgcaaccc tggcacgtcg tagcgttgat atttttcaga attatgttgc cattgccctg 1440

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cgtgcctgtc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

cagaaaccga cctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgtgtctgca t 1701

<210> 8
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 8

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Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys
            20                  25                  30

Leu Thr Ile Asn Asp Val Ala Arg Val Ala Arg Asn Gly Thr Leu Val
        35                  40                  45

Ser Leu Thr Asn Asn Thr Asp Ile Leu Gln Gly Ile Gln Ala Ser Cys
    50                  55                  60

Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val
65                  70                  75                  80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Ala Ile Ser Arg Glu Gln
                85                  90                  95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
            100                 105                 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
        115                 120                 125

Ala Asn Ser His Met Arg Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
    130                 135                 140

Lys Arg Met Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145                 150                 155                 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
                165                 170                 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
            180                 185                 190
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Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
        195                 200                 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
    210                 215                 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225                 230                 235                 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
                245                 250                 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
            260                 265                 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
        275                 280                 285

Ala Asn Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
    290                 295                 300

Arg Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
                325                 330                 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
        355                 360                 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Leu Leu Ala Lys
    370                 375                 380
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His Leu Asp Val Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385                 390                 395                 400


Gly Leu Pro Pro Ser Leu Leu Gly Asn Arg Glu Arg Lys Val Asn Met
                405                 410                 415


Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430


Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445


Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
    450                 455                 460


Ala Arg Arg Ser Val Asp Ile Phe Gln Asn Tyr Val Ala Ile Ala Leu
465                 470                 475                 480


Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
                485                 490                 495


His Tyr Asp Ala Arg Ala Cys Leu Ser Pro Ala Thr Glu Arg Leu Tyr
            500                 505                 510


Ser Ala Val Arg His Val Val Gly Gln Lys Pro Thr Ser Asp Arg Pro
        515                 520                 525


Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
    530                 535                 540


Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545                 550                 555                 560


Asp Ile Leu Pro Cys Leu His
                565
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<210> 9
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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caggccagct gtgattatat caataatgca gttgaaagcg gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc gtggtgcaag cggtattcgt 420

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agcgcaaccc tggcacgtcg tagcgttgat atttttcaga attatgttgc cattgccctg 1440

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cgtgcctgtc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

cagaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgtgtctgca t 1701

<210> 10
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 10

Met Lys Thr Leu Ser Gln Ala Gln Ser Lys Thr Ser Ser Gln Gln Phe
1 5 10 15

Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys
20 25 30

Leu Thr Ile Asn Asp Val Val Arg Val Ala Arg Asn Gly Thr Leu Val
35 40 45

Ser Leu Thr Asn Asn Thr Asp Ile Leu Gln Gly Ile Gln Ala Ser Cys
50 55 60

Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val

65 70 75 80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
85 90 95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
100 105 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
115 120 125

Ala Asn Ser His Met Arg Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
130 135 140

Lys Arg Met Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145 150 155 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
165 170 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
180 185 190

Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
195 200 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
210 215 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225 230 235 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
245 250 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys

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            260                 265                 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
        275                 280                 285

Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
    290                 295                 300

Arg Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
                325                 330                 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
        355                 360                 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Leu Leu Ala Lys
    370                 375                 380

His Leu Asp Val Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385                 390                 395                 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
                405                 410                 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430

Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
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    450                 455                 460

Ala Arg Arg Ser Val Asp Ile Phe Gln Asn Tyr Val Ala Ile Ala Leu
465                 470                 475                 480

Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
                485                 490                 495

His Tyr Asp Ala Arg Ala Cys Leu Ser Pro Ala Thr Glu Arg Leu Tyr
            500                 505                 510

Ser Ala Val Arg His Val Val Gly Gln Lys Pro Ser Ser Asp Arg Pro
        515                 520                 525

Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
    530                 535                 540

Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545                 550                 555                 560

Asp Ile Leu Pro Cys Leu His
                565
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<210> 11
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 11

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gttgcccgta atggcaccct ggttagcctg accaataata aagatattct gcagcgtatt      180

caggccagct gtgattatat caataatgca gttgaaaaag gtgaaccgat ttatggtgtt      240
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accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc gtggtgcaag cggtattcgt 420

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cgtgcccagc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

aaaaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgccgctgca t 1701

<210> 12
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 12

Met Lys Thr Leu Ser Gln Ala Gln Ser Lys Thr Ser Ser Gln Gln Phe
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Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys
20 25 30

Leu Thr Ile Asn Asp Val Val Arg Val Ala Arg Asn Gly Thr Leu Val
35 40 45

Ser Leu Thr Asn Asn Lys Asp Ile Leu Gln Arg Ile Gln Ala Ser Cys
50 55 60

Asp Tyr Ile Asn Asn Ala Val Glu Lys Gly Glu Pro Ile Tyr Gly Val
65 70 75 80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
85 90 95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
100 105 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
115 120 125

Ala Asn Ser His Met Arg Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
130 135 140

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Lys Arg Met Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145                 150                 155                 160


Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
                165                 170                 175


Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
            180                 185                 190


Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
        195                 200                 205


Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
    210                 215                 220


Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225                 230                 235                 240


Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
                245                 250                 255


Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
            260                 265                 270


Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
        275                 280                 285


Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
    290                 295                 300


Met Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320


Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
                325                 330                 335
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Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
        355                 360                 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Leu Leu Ala Lys
    370                 375                 380

His Leu Asp Val Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385                 390                 395                 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
                405                 410                 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430

Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
    450                 455                 460

Ala Arg Arg Ser Val Asp Ile Phe Gln Asn Tyr Val Ala Ile Ala Leu
465                 470                 475                 480

Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
                485                 490                 495

His Tyr Asp Ala Arg Ala Gln Leu Ser Pro Ala Thr Glu Arg Leu Tyr
            500                 505                 510

Ser Ala Val Arg His Val Val Gly Lys Lys Pro Ser Ser Asp Arg Pro
        515                 520                 525
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Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
530 535 540

Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545 550 555 560

Asp Ile Leu Pro Pro Leu His
565

<210> 13
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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gttgcccgta atggcaccct ggttagcctg accaataata aagatattct gcagcgtatt 180

caggccagct gtgattatat caataatgca gttgaaagcg gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc gtggtgcaag cggtattcgt 420

ctggaactga ttaaacgcat ggaaatcttt ctgaatgccg gtgttacccc gtatgtttat 480

gaatttggta gcattggtgc cagcggtgat ctggttccgc tgagctatat taccggtagc 540

ctgattggcc tggacccgag ctttaaagtt gattttaatg gcaaagaaat ggacgcaccg 600

accgcactgc gtcagctgaa tctgagtccg ctgaccctgc tgccgaaaga aggtctggca 660

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ggtaattttc tgggtcagta tgttggtatg ggtatggatc atctgcgcta ttatatcggt 1140

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ggtctgcctc cgagtctggt gggtaatcgt gaacgtaaag ttaatatggg tctgaaaggt 1260

ctgcagattt gcggtaatag cattatgccg ctgctgacct tttatggtaa tagtattgca 1320

gatcgttttc cgacccatgc cgaacagttt aaccagaata ttaacagcca gggttatacc 1380

agcgcaaccc tggcacgtcg tagcgttgat atttttcaga attatgttgc cattgccctg 1440

atgtttggtg ttcaggcagt tgatctgcgt acctacaaaa aaaccggtca ttatgatgca 1500

cgtgcccagc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

aaaaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

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<210> 14
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 14

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Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys

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            20                  25                  30

Leu Thr Ile Asn Asp Val Val Arg Val Ala Arg Asn Gly Thr Leu Val
        35                  40                  45

Ser Leu Thr Asn Asn Lys Asp Ile Leu Gln Arg Ile Gln Ala Ser Cys
    50                  55                  60

Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val
65                  70                  75                  80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
                85                  90                  95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
            100                 105                 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
        115                 120                 125

Ala Asn Ser His Met Arg Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
    130                 135                 140

Lys Arg Met Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145                 150                 155                 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
                165                 170                 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
            180                 185                 190

Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
        195                 200                 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
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210 215 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225 230 235 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
245 250 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
260 265 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
275 280 285

Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
290 295 300

Met Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305 310 315 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
325 330 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
340 345 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
355 360 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Leu Leu Ala Lys
370 375 380

His Leu Asp Val Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385 390 395 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met

405 410 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
420 425 430

Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
435 440 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
450 455 460

Ala Arg Arg Ser Val Asp Ile Phe Gln Asn Tyr Val Ala Ile Ala Leu
465 470 475 480

Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
485 490 495

His Tyr Asp Ala Arg Ala Gln Leu Ser Pro Ala Thr Glu Arg Leu Tyr
500 505 510

Ser Ala Val Arg His Val Val Gly Lys Lys Pro Ser Ser Asp Arg Pro
515 520 525

Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
530 535 540

Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545 550 555 560

Asp Ile Leu Pro Asn Leu His
565

<210> 15
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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gttgcccgta atggcaccct ggttagcctg accaataata ccgatattct gcagggtatt 180

caggccagct gtgattatat caataatgca gttgaaagcg gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc atggtgcaag cggtattcgt 420

ctggaactga ttaaacgcgc ggaaatcttt ctgaatgccg gtgttacccc gtatgtttat 480

gaatttggta gcattggtgc cagcggtgat ctggttccgc tgagctatat taccggtagc 540

ctgattggcc tggacccgag ctttaaagtt gattttaatg gcaaagaaat ggacgcaccg 600

accgcactgc gtcagctgaa tctgagtccg ctgaccctgc tgccgaaaga aggtctggca 660

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ggtctgcctc cgagtctggt gggtaatcgt gaacgtaaag ttaatatggg tctgaaaggt 1260

ctgcagattt gcggtaatag cattatgccg ctgctgacct tttatggtaa tagtattgca 1320

gatcgttttc cgacccatgc cgaacagttt aaccagaata ttaacagcca gggttatacc 1380

agcgcaaccc tggcacgtcg tagcgttgat attggccaga attatgttgc cattgccctg 1440

atgtttggtg ttcaggcagt tgatctgcgt acctacaaaa aaaccggtca ttatgatgca 1500

cgtgcccagc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

cagaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgaacctgca t 1701

<210> 16
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 16

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Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys
20 25 30

Leu Thr Ile Asn Asp Val Ala Arg Val Ala Arg Asn Gly Thr Leu Val
35 40 45

Ser Leu Thr Asn Asn Thr Asp Ile Leu Gln Gly Ile Gln Ala Ser Cys
50 55 60

Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val
65 70 75 80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
85 90 95

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Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
            100                 105                 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
        115                 120                 125

Ala Asn Ser His Met His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
    130                 135                 140

Lys Arg Ala Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145                 150                 155                 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
                165                 170                 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
            180                 185                 190

Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
        195                 200                 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
    210                 215                 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225                 230                 235                 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
                245                 250                 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
            260                 265                 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
        275                 280                 285
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Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
    290                 295                 300

Arg Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
                325                 330                 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
        355                 360                 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Gly Leu Ala Lys
    370                 375                 380

His Leu Asp Val Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385                 390                 395                 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
                405                 410                 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430

Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
    450                 455                 460

Ala Arg Arg Ser Val Asp Ile Gly Gln Asn Tyr Val Ala Ile Ala Leu
465                 470                 475                 480
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Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
485 490 495

His Tyr Asp Ala Arg Ala Gln Leu Ser Pro Ala Thr Glu Arg Leu Tyr
500 505 510

Ser Ala Val Arg His Val Val Gly Gln Lys Pro Ser Ser Asp Arg Pro
515 520 525

Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
530 535 540

Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545 550 555 560

Asp Ile Leu Pro Asn Leu His
565

<210> 17
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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caggccagct gtgattatat caataatgca gttgaaagcg gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc atggtgcaag cggtattcgt 420

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atgtttggtg ttcaggcagt tgatctgcgt acctacaaaa aaaccggtca ttatgatgca 1500

cgtgcccagc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

cagaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgaacctgca t 1701

<210> 18
<211> 567
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 18

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Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys
            20                  25                  30


Leu Thr Ile Asn Asp Val Ala Arg Val Ala Arg Asn Gly Thr Leu Val
        35                  40                  45


Ser Leu Thr Asn Asn Thr Asp Ile Leu Gln Gly Ile Gln Ala Ser Cys
    50                  55                  60


Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val
65                  70                  75                  80


Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
                85                  90                  95


Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
            100                 105                 110


Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
        115                 120                 125


Ala Asn Ser His Met His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
    130                 135                 140


Lys Arg Ala Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145                 150                 155                 160


Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
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                165                 170                 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
            180                 185                 190

Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
        195                 200                 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
    210                 215                 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225                 230                 235                 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
                245                 250                 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
            260                 265                 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
        275                 280                 285

Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
    290                 295                 300

Arg Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
                325                 330                 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
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        355                 360                 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Gly Leu Ala Lys
    370                 375                 380

His Leu Asp Thr Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385                 390                 395                 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
                405                 410                 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430

Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
    450                 455                 460

Ala Arg Arg Ser Val Asp Ile Gly Gln Asn Tyr Val Ala Ile Ala Leu
465                 470                 475                 480

Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
                485                 490                 495

His Tyr Asp Ala Arg Ala Gln Leu Ser Pro Ala Thr Glu Arg Leu Tyr
            500                 505                 510

Ser Ala Val Arg His Val Val Gly Gln Lys Pro Ser Ser Asp Arg Pro
        515                 520                 525

Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
    530                 535                 540

Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
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545 550 555 560

Asp Ile Leu Pro Asn Leu His
565

<210> 19
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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caggccagct gtgattatat caataatgca gttgaaagcg gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc atggtgcaag cggtattcgt 420

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agcgcaaccc tggcacgtcg tagcgttgat attggccaga attatgttgc cattgccctg 1440

atgtttggtg ttcaggcagt tgatctgcgt acctacaaaa aaaccggtca ttatgatgca 1500

cgtgcccagc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

cagaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgaacctgca t 1701

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<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 20

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Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys
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Leu Thr Ile Asn Asp Val Ala Arg Val Ala Arg Asn Gly Thr Leu Val
35 40 45

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Ser Leu Thr Asn Asn Thr Asp Ile Leu Gln Gly Ile Gln Ala Ser Cys
    50                  55                  60

Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val
65                  70                  75                  80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
                85                  90                  95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
            100                 105                 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
        115                 120                 125

Ala Asn Ser His Met His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
    130                 135                 140

Lys Arg Ala Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145                 150                 155                 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
                165                 170                 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
            180                 185                 190

Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
        195                 200                 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
    210                 215                 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225                 230                 235                 240
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Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
                245                 250                 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
            260                 265                 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
        275                 280                 285

Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
    290                 295                 300

Arg Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
                325                 330                 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
        355                 360                 365

Gly Met Gly Met Asp His Leu Arg Tyr Glu Ile Gly Leu Leu Ala Lys
    370                 375                 380

His Leu Asp Val Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385                 390                 395                 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
                405                 410                 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430
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Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445


Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
    450                 455                 460


Ala Arg Arg Ser Val Asp Ile Gly Gln Asn Tyr Val Ala Ile Ala Leu
465                 470                 475                 480


Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
                485                 490                 495


His Tyr Asp Ala Arg Ala Gln Leu Ser Pro Ala Thr Glu Arg Leu Tyr
            500                 505                 510


Ser Ala Val Arg His Val Val Gly Gln Lys Pro Ser Ser Asp Arg Pro
        515                 520                 525


Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
    530                 535                 540


Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545                 550                 555                 560


Asp Ile Leu Pro Asn Leu His
                565


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<211>  1701
<212>  DNA
<213>  Artificial Sequence

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<223>  Synthetic polynucleotide

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caggccagct gtgattatat caataatgca gttgaaagcg gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc atggtgcaag cggtattcgt 420

ctggaactga ttaaacgcgc ggaaatcttt ctgaatgccg gtgttacccc gtatgtttat 480

gaatttggta gcattggtgc cagcggtgat ctggttccgc tgagctatat taccggtagc 540

ctgattggcc tggacccgag ctttaaagtt gattttaatg gcaaagaaat ggacgcaccg 600

accgcactgc gtcagctgaa tctgagtccg ctgaccctgc tgccgaaaga aggtctggca 660

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cgtgcccagc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

cagaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgaacctgca t 1701

<210> 22
<211> 567
<212> PRT
<213> Artificial Sequence

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<223> Synthetic polypeptide

<400> 22

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Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys
20 25 30

Leu Thr Ile Asn Asp Val Ala Arg Val Ala Arg Asn Gly Thr Leu Val
35 40 45

Ser Leu Thr Asn Asn Thr Asp Ile Leu Gln Gly Ile Gln Ala Ser Cys
50 55 60

Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val
65 70 75 80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
85 90 95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
100 105 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg

115 120 125

Ala Asn Ser His Met His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
130 135 140

Lys Arg Ala Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145 150 155 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
165 170 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
180 185 190

Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
195 200 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
210 215 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225 230 235 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
245 250 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
260 265 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
275 280 285

Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
290 295 300

Arg Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro

305 310 315 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
325 330 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
340 345 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
355 360 365

Gly Met Gly Met Asp His Leu Arg Tyr Glu Ile Gly Leu Leu Ala Lys
370 375 380

His Leu Asp Thr Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385 390 395 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
405 410 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
420 425 430

Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
435 440 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
450 455 460

Ala Arg Arg Ser Val Asp Ile Gly Gln Asn Tyr Val Ala Ile Ala Leu
465 470 475 480

Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
485 490 495

His Tyr Asp Ala Arg Ala Gln Leu Ser Pro Ala Thr Glu Arg Leu Tyr

500 505 510

Ser Ala Val Arg His Val Val Gly Gln Lys Pro Ser Ser Asp Arg Pro
515 520 525

Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
530 535 540

Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545 550 555 560

Asp Ile Leu Pro Asn Leu His
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<210> 23
<211> 1701
<212> DNA
<213> Artificial Sequence

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<223> Synthetic polynucleotide

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gttgcccgta atggcaccgc ggttagcctg accaataata aagatattct gcagcgtatt 180

caggccagct gtgattatat caataatgca gttgaaaaag gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc gtggtgcaag cggtattcgt 420

ctggaactga ttaaacgcat ggaaatcttt ctgaatgccg gtgttacccc gtatgtttat 480

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ctgcagattt gcggtaatag cattatgccg ctgctgacct tttatggtaa tagtattgca 1320

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cgtgcccagc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

aaaaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgccgctgca t 1701

<210> 24
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 24

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            20                  25                  30

Leu Thr Ile Asn Asp Val Val Arg Val Ala Arg Asn Gly Thr Ala Val
        35                  40                  45

Ser Leu Thr Asn Asn Lys Asp Ile Leu Gln Arg Ile Gln Ala Ser Cys
    50                  55                  60

Asp Tyr Ile Asn Asn Ala Val Glu Lys Gly Glu Pro Ile Tyr Gly Val
65                  70                  75                  80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
                85                  90                  95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
            100                 105                 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
        115                 120                 125

Ala Asn Ser His Met Arg Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
    130                 135                 140

Lys Arg Met Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145                 150                 155                 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
                165                 170                 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
            180                 185                 190
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Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
        195                 200                 205

Ser Pro Leu Thr Leu Gln Pro Lys Glu Gly Leu Ala Met Met Asn Gly
    210                 215                 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225                 230                 235                 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
                245                 250                 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys
            260                 265                 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
        275                 280                 285

Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
    290                 295                 300

Met Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
                325                 330                 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
        355                 360                 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Leu Leu Ala Lys
    370                 375                 380
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```
His Leu Asp Val Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385                 390                 395                 400


Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
                405                 410                 415


Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430


Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445


Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
    450                 455                 460


Ala Arg Arg Ser Val Asp Ile Phe Gln Asn Tyr Val Ala Ile Ala Leu
465                 470                 475                 480


Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
                485                 490                 495


His Tyr Asp Ala Arg Ala Gln Leu Ser Pro Ala Thr Glu Arg Leu Tyr
            500                 505                 510


Ser Ala Val Arg His Val Val Gly Lys Lys Pro Ser Ser Asp Arg Pro
        515                 520                 525


Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
    530                 535                 540


Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545                 550                 555                 560


Asp Ile Leu Pro Pro Leu His
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<210> 25
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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caggccagct gtgattatat caataatgca gttgaaagcg gtgaaccgat ttatggtgtt 240

accagcggtt ttggtggtat ggcaaatgtt gtaattagcc gtgaacaggc aagcgaactg 300

cagaccaatc tggtttggtt tctgaaaacc ggtgcaggta ataaactgcc gctggcagat 360

gttcgtgcag caatgctgct gcgtgcaaat agccacatgc gtggtgcaag cggtattcgt 420

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cgtgcccagc tgtcaccggc aaccgaacgt ctgtatagcg cagttcgtca tgttgttggt 1560

cagaaaccga gctcagatcg tccgtatatt tggaatgata atgaacaggg tctggatgaa 1620

catattgcac gtattagtgc agatattgca gccggtggtg ttattgttca ggccgttcag 1680

gacattctgc cgaacctgca t 1701

<210> 26
<211> 567
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 26

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Ser Phe Thr Gly Asn Ser Ser Ala Asn Val Ile Ile Gly Asn Gln Lys
20 25 30

Leu Thr Ile Asn Asp Val Ala Arg Val Ala Arg Asn Gly Thr Leu Val
35 40 45

Ser Leu Thr Asn Asn Thr Asp Ile Leu Gln Gly Ile Gln Ala Ser Cys
50 55 60

Asp Tyr Ile Asn Asn Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val

65 70 75 80

Thr Ser Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Arg Glu Gln
85 90 95

Ala Ser Glu Leu Gln Thr Asn Leu Val Trp Phe Leu Lys Thr Gly Ala
100 105 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
115 120 125

Ala Asn Ser His Met Arg Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
130 135 140

Lys Arg Ala Glu Ile Phe Leu Asn Ala Gly Val Thr Pro Tyr Val Tyr
145 150 155 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
165 170 175

Ile Thr Gly Ser Leu Ile Gly Leu Asp Pro Ser Phe Lys Val Asp Phe
180 185 190

Asn Gly Lys Glu Met Asp Ala Pro Thr Ala Leu Arg Gln Leu Asn Leu
195 200 205

Ser Pro Leu Thr Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
210 215 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Thr Gln
225 230 235 240

Ile Leu Thr Ala Ile Ala Met Gly Val His Ala Leu Asp Ile Gln Ala
245 250 255

Leu Asn Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Asn Ser Lys

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            260                 265                 270

Pro His Pro Gly Gln Leu Trp Ala Ala Asp Gln Met Ile Ser Leu Leu
        275                 280                 285

Ala Gly Ser Gln Leu Val Arg Asp Glu Leu Asp Gly Lys His Asp Tyr
    290                 295                 300

Arg Asp Gly Glu Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320

Gln Tyr Leu Gly Pro Ile Val Asp Gly Ile Ser Gln Ile Ala Lys Gln
                325                 330                 335

Ile Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Asp Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
        355                 360                 365

Gly Met Gly Met Asp His Leu Arg Tyr Tyr Ile Gly Gly Leu Ala Lys
    370                 375                 380

His Leu Asp Val Gln Ile Ala Leu Leu Ala Ser Pro Glu Phe Ser Asn
385                 390                 395                 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Arg Glu Arg Lys Val Asn Met
                405                 410                 415

Gly Leu Lys Gly Leu Gln Ile Cys Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430

Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Thr Ser Ala Thr Leu
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    450                 455                 460

Ala Arg Arg Ser Val Asp Ile Gly Gln Asn Tyr Val Ala Ile Ala Leu
465                 470                 475                 480

Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Lys Thr Gly
                485                 490                 495

His Tyr Asp Ala Arg Ala Gln Leu Ser Pro Ala Thr Glu Arg Leu Tyr
            500                 505                 510

Ser Ala Val Arg His Val Val Gly Gln Lys Pro Ser Ser Asp Arg Pro
        515                 520                 525

Tyr Ile Trp Asn Asp Asn Glu Gln Gly Leu Asp Glu His Ile Ala Arg
    530                 535                 540

Ile Ser Ala Asp Ile Ala Ala Gly Gly Val Ile Val Gln Ala Val Gln
545                 550                 555                 560

Asp Ile Leu Pro Asn Leu His
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<213>  Artificial Sequence

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1781)..(1781)
<223> n is a, c, g, or t

<220>
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<220>
<221> misc_feature
<222> (1786)..(1786)
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atcggctgct tttttttgn nngaggttcc aacttgtggt ataatgaaat aagatcactc 180

cggagcgtat tttttgagtt atcgagattt tcaggagcta aggaggaact aaaatggaga 240

aaaaaatcac tggatatacc accgttgata tatcccaatg gcatcgtaaa gaacattttg 300

aggcatttca gtcagttgct caatgtacct ataaccagac cgttcagctg gatattacgg 360

ccttttaaa gaccgtaaag aaaaataagc acaagtttta tccggccttt attcacattc 420

ttgcccgcct gatgaatgct catccggagt tccgtatggc aatgaaagac ggtgagctgg 480

tgatatggga tagtgttcac ccttgttaca ccgttttcca tgagcaaact gaaacgtttt 540

catcgctctg gagtgaatac cacgacgatt tccggcagtt tctacacata tattcgcaag 600

atgtggcgtg ttacggtgaa aacctggcct atttccctaa agggtttatt gagaatatgt 660

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tgctgatgcc gctggcgatt caggttcatc atgccgtctg tgatggcttc catgtcggca 840

gaatgcttaa tgaattacaa cagtactgcg atgagtggca gggcggggcg taactgcagg 900

agctcaaaca gcagcctgta ttcaggctgc ttttttcgtt ttggtctgcg cgtaatctct 960

tgctctgaaa acgaaaaaac cgccttgcag ggcggttttt cgaaggttct ctgagctacc 1020

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taaggcgcag cggtcggact gaacgggggg ttcgtgcata cagtccagct tggagcgaac 1260

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tgacaccggt aaaccgaaag gcaggaacag gagagcgcac gagggagccg ccaggggaa 1380

acgcctggta tctttatagt cctgtcgggt ttcgccacca ctgatttgag cgtcagattt 1440

cgtgatgctt gtcaggggg cggagcctat ggaaaaacgg ctttgccgcg gccctctcac 1500

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cacaacaact ggcgggcaaa cagtcgttgc tgattggcgt tgccacctcc agtctggccc 2040

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tgaatgaggg catcgttccc actgcgatgc tggttgccaa cgatcagatg gcgctgggcg 2580

caatgcgcgc cattaccgag tccgggctgc gcgttggtgc ggacatctcg gtagtgggat 2640

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tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 3060

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gccgtcgttt tacaatctag aggccagcct ggccataagg agatatacat atgggccatc 3180

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gcgcaaatgt gattattggt aatcagaaac tgaccatcaa tgatgttgca cgtgttgccc 3360

gtaatggcac cctggttagc ctgaccaata ataccgatat tctgcagggt attcaggcca 3420

gctgtgatta tatcaataat gcagttgaaa gcggtgaacc gatttatggt gttaccagcg 3480

gttttggtgg tatggcaaat gttgcaatta gccgtgaaca ggcaagcgaa ctgcagacca 3540

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gctttcatcc gtttatccat aacagcaaac cgcatccggg tcagctgtgg gcagcagatc 4080

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<211> 56

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 28
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<210> 29
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 29
gatggtgatg gtggccagtt tggccttaat gcagacacgg cagaatg 47

<210> 30
<211> 569
<212> PRT
<213> Nostoc punctiforme

<400> 30

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Pro Phe Thr Asn Ser Ser Asp Ser Ile Val Thr Val Gly Asp Arg Asn
20 25 30

Leu Thr Ile Asp Glu Val Val Asn Val Ala Arg His Gly Thr Gln Val
35 40 45

Arg Leu Thr Asp Asn Ala Asp Val Ile Arg Gly Val Gln Ala Ser Cys
50 55 60

Asp Tyr Ile Asn Asn Ala Val Glu Thr Ala Gln Pro Ile Tyr Gly Val
65 70 75 80

```
Thr Ser Gly Phe Gly Gly Met Ala Asp Val Val Ile Ser Arg Glu Gln
                85                  90                  95

Ala Ala Glu Leu Gln Thr Asn Leu Ile Trp Phe Leu Lys Ser Gly Ala
            100                 105                 110

Gly Asn Lys Leu Ser Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
        115                 120                 125

Ala Asn Ser His Leu Tyr Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
    130                 135                 140

Gln Arg Ile Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Tyr
145                 150                 155                 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
                165                 170                 175

Ile Thr Gly Ala Leu Ile Gly Leu Asp Pro Ser Phe Thr Val Asp Phe
            180                 185                 190

Asp Gly Lys Glu Met Asp Ala Val Thr Ala Leu Ser Arg Leu Gly Leu
        195                 200                 205

Pro Lys Leu Gln Leu Gln Pro Lys Glu Gly Leu Ala Met Met Asn Gly
    210                 215                 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Lys
225                 230                 235                 240

Val Leu Leu Ala Leu Thr Met Gly Val His Ala Leu Ala Ile Gln Gly
                245                 250                 255

Leu Tyr Gly Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys
            260                 265                 270
```

```
Pro His Pro Gly Gln Leu Trp Thr Ala Asp Gln Met Phe Ser Leu Leu
        275                 280                 285

Lys Asp Ser Ser Leu Val Arg Glu Glu Leu Asp Gly Lys His Glu Tyr
    290                 295                 300

Arg Gly Lys Asp Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Ala
305                 310                 315                 320

Gln Phe Ile Gly Pro Ile Val Asp Gly Val Ser Glu Ile Thr Lys Gln
                325                 330                 335

Ile Glu Val Glu Met Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Glu Asn Gln Val Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val
        355                 360                 365

Gly Val Thr Met Asp Arg Leu Arg Tyr Tyr Ile Gly Leu Leu Ala Lys
    370                 375                 380

His Ile Asp Val Gln Ile Ala Leu Leu Val Ser Pro Glu Phe Ser Asn
385                 390                 395                 400

Gly Leu Pro Pro Ser Leu Val Gly Asn Ser Asp Arg Lys Val Asn Met
                405                 410                 415

Gly Leu Lys Gly Leu Gln Ile Ser Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430

Ser Phe Tyr Gly Asn Ser Leu Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445

Gln Phe Asn Gln Asn Ile Asn Ser Gln Gly Tyr Ile Ser Ala Asn Leu
    450                 455                 460
```

```
Thr Arg Arg Ser Val Asp Ile Phe Gln Asn Tyr Met Ala Ile Ala Leu
465                 470                 475                 480


Met Phe Gly Val Gln Ala Val Asp Leu Arg Thr Tyr Lys Met Lys Gly
                485                 490                 495


His Tyr Asp Ala Arg Thr Cys Leu Ser Pro Asn Thr Val Gln Leu Tyr
            500                 505                 510


Thr Ala Val Cys Glu Val Val Gly Lys Pro Leu Thr Ser Val Arg Pro
        515                 520                 525


Tyr Ile Trp Asn Asp Asn Glu Gln Cys Leu Asp Glu His Ile Ala Arg
    530                 535                 540


Ile Ser Ala Asp Ile Ala Gly Gly Gly Leu Ile Val Gln Ala Val Glu
545                 550                 555                 560


His Ile Phe Ser Ser Leu Lys Ser Thr
                565


<210>  31
<211>  571
<212>  PRT
<213>  Rivularia sp. PCC 7116

<400>  31

Met Asn Thr Val Arg Leu Thr Lys Asn Thr Val Ser Gln Lys Ser Phe
1               5                   10                  15


Ser Phe Leu Asn Asn Ser Asp Ala Ser Val Ile Val Gly Asp Arg Gln
            20                  25                  30


Leu Thr Ile Glu Glu Val Val Ser Val Ala Arg Tyr Arg Ala Arg Val
        35                  40                  45
```

```
Lys Leu Thr Glu Asn Leu Glu Lys Leu Ala Asn Val Gln Ala Ser Cys
    50                  55                  60

Asp Phe Ile Arg Asp Ala Val Glu Ser Gly Glu Pro Ile Tyr Gly Val
65                  70                  75                  80

Thr Thr Gly Phe Gly Gly Met Ala Asn Val Val Ile Ser Pro Glu Ser
                85                  90                  95

Ala Thr Leu Leu Gln Asn Asn Leu Met Cys Tyr His Lys Val Gly Ala
            100                 105                 110

Gly Asn Lys Leu Pro Leu Ala Asp Val Arg Ala Ala Met Leu Leu Arg
        115                 120                 125

Ala Asn Ser His Val Ala Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile
    130                 135                 140

Lys Arg Met Leu Ile Phe Leu Asn Ala Gly Val Thr Pro His Val Pro
145                 150                 155                 160

Glu Phe Gly Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr
                165                 170                 175

Ile Ser Gly Ala Leu Ile Gly Leu Asn Ser Ser Tyr Ile Val Asp Phe
            180                 185                 190

Asp Gly Glu Glu Met Asp Ala Pro Thr Ala Leu Gln Lys Leu Gly Leu
        195                 200                 205

Glu Pro Leu Gln Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly
    210                 215                 220

Thr Ser Val Met Thr Gly Ile Ala Ala Asn Cys Val Gln Asp Thr Arg
225                 230                 235                 240
```

```
Ile Leu Leu Ala Leu Ser Val Ala Thr His Ala Leu Thr Ile Gln Gly
                245                 250                 255

Leu Glu Gly Thr Asn Gln Ser Phe His Glu Tyr Ile His Lys Leu Lys
            260                 265                 270

Pro His Ser Gly Gln Ile Trp Ala Ala Ser Gln Met Leu Glu Leu Leu
        275                 280                 285

Ala Gly Ser Gly Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr
    290                 295                 300

Arg Gly Lys Asn Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro
305                 310                 315                 320

Gln Tyr Met Gly Pro Ile Val Asp Gly Ile Glu Asp Ile Ala Lys Gln
                325                 330                 335

Val Glu Ile Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val
            340                 345                 350

Glu Asn Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile
        355                 360                 365

Gly Val Gly Met Asp Arg Leu Arg Tyr His Ile Gly Met Leu Ala Lys
    370                 375                 380

His Leu Asp Val Gln Ile Ala Tyr Leu Val Ala Pro Glu Phe Asn Asn
385                 390                 395                 400

Gly Leu Ser Pro Ser Leu Val Gly Asn Gln Gln Arg Thr Val Asn Met
                405                 410                 415

Gly Leu Lys Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu
            420                 425                 430
```

```
Thr Phe Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu
        435                 440                 445

Gln Tyr Asn Gln Asn Ile Asn Ser Gln Gly Phe Ala Ser Ala Asn Leu
    450                 455                 460

Ala Arg Thr Ser Val Glu Ile Phe Gln Gln Tyr Ile Ala Leu Ala Leu
465                 470                 475                 480

Met Phe Gly Val Gln Ser Val Asp Leu Arg Thr Tyr Ala Ile Ala Gly
                485                 490                 495

His Tyr Asp Ala Arg Ala Thr Leu Ser Pro Ala Thr Gln Asp Leu Tyr
            500                 505                 510

Met Ala Val Arg Asn Val Val Gly Arg Pro Pro Ser Lys Glu Arg Ala
        515                 520                 525

Tyr Ile Trp Asp Asp Asn Glu Gln Gly Leu Asp Ser His Ile Ser Lys
    530                 535                 540

Ile Ala Asp Asp Ile Ala Tyr Gly Gly Gln Ile Val Thr Ala Ile Ser
545                 550                 555                 560

Glu Val Leu Ser Ala Leu Lys Ser Val Asn Asn
                565                 570
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<210> 32
<211> 565
<212> PRT
<213> Oscillatoria sp. PCC 6506

<400> 32

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Met Ser Thr Asn Leu Thr Glu Pro Ile Ser Gln Lys Leu Leu Gln Trp
1               5                   10                  15

Leu Glu Pro Asn Leu Ser Ala Val Ile Val Gly Asn Arg Arg Leu Ser
```

```
            20                  25                  30

Val Glu Glu Val Ala Arg Val Ala Arg Cys Gly Thr Arg Val Arg Leu
        35                  40                  45

Asn Asp Glu Ser Asp Val Ala Glu Arg Val Gln Ala Ser Cys Asp Tyr
    50                  55                  60

Ile Thr Asp Ala Val Glu Ser Gly Lys Ala Ile Tyr Gly Val Thr Thr
65                  70                  75                  80

Gly Phe Gly Gly Met Ala Asn Thr Glu Ile Ala Pro Glu Glu Ala Ala
                85                  90                  95

Ser Leu Gln Asn Asn Leu Ile Trp Phe Leu Lys Ala Gly Ala Gly Gln
            100                 105                 110

Lys Leu Pro Thr Ala Cys Val Arg Ala Ala Met Leu Leu Arg Ile Asn
        115                 120                 125

Ser His Leu Gln Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Lys Arg
    130                 135                 140

Met Ile Val Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Leu
145                 150                 155                 160

Gly Ser Ile Gly Ala Ser Gly Asp Leu Val Pro Leu Ala Gln Ile Thr
                165                 170                 175

Gly Ala Leu Ile Gly Leu Asp Asp Ser Phe Thr Val Asp Phe Asn Gly
            180                 185                 190

Arg Glu Met Ser Ala Ile Gln Ala Leu Glu Leu Leu Asp Leu Pro Lys
        195                 200                 205

Ile Asp Leu Arg Pro Lys Glu Gly Leu Ala Met Val Asn Gly Thr Ser
```

210 215 220

Val Met Thr Gly Ile Ala Ala Asn Cys Val Arg Asp Ser Gln Val Met
225 230 235 240

Leu Ala Leu Ala Met Gly Thr His Ala Leu Met Ile Gln Gly Leu Gly
245 250 255

Ala Thr Asn Gln Ser Phe His Pro Phe Ile His Lys Leu Lys Pro His
260 265 270

Phe Gly Gln Val Trp Ala Ala Ser Gln Met Val Glu Leu Leu Ala Gly
275 280 285

Ser Cys Leu Asn Arg Asp Glu Leu Asp Gly Gln His Asp Ala Arg Gly
290 295 300

Glu His Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr
305 310 315 320

Ile Gly Pro Ile Val Asp Gly Ile Ala Glu Ile Ala Gln Gln Ile Glu
325 330 335

Val Glu Val Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Thr Glu Asn
340 345 350

Gln Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Val Gly Val
355 360 365

Gly Met Asp Arg Leu Arg Tyr Leu Leu Gly Leu Leu Ala Lys His Leu
370 375 380

Asp Val Gln Ile Ala Leu Leu Ala Ala Pro Glu Phe Asn Asn Gly Leu
385 390 395 400

Ser Pro Ser Leu Val Gly Asn Thr Ser Arg Lys Val Asn Met Gly Leu

405 410 415

Lys Gly Leu Gln Ile Ala Gly Asn Ser Ile Met Pro Leu Leu Thr Phe
420 425 430

Tyr Gly Asn Ser Ile Ala Asp Arg Phe Pro Thr His Ala Glu Gln Phe
435 440 445

Asn Gln Asn Ile Asn Ser Gln Gly Phe Ala Ser Ala Asn Leu Ala Arg
450 455 460

Arg Ser Ile Glu Leu Phe Gln Gln Tyr Met Ala Ile Ser Leu Met Phe
465 470 475 480

Ala Val Gln Ala Val Asp Leu Arg Thr His Glu Val Ala Gly His Tyr
485 490 495

Asp Ala Arg Glu Cys Leu Ser Pro Leu Ser Leu Pro Leu Tyr Glu Ala
500 505 510

Val Arg Glu Val Val Gly Gln Pro Pro Asn Val Asp Arg Ser Tyr Ile
515 520 525

Trp Asn Asp Asn Glu Gln Ser Leu Asp Ile His Ile Ala Met Ile Ala
530 535 540

Ala Asp Ile Ala Gln Glu Gly Arg Ile Val Gln Ala Val Asn Gln Ile
545 550 555 560

Leu Ser Ser Leu Lys
565

<210> 33
<211> 559
<212> PRT
<213> Gloeocapsa sp. PCC 7428

<400> 33

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Met Asn Thr Ala Val Gln Thr Gln Ala Ser Thr Asn Leu Asn Ala Asp
1               5                   10                  15

Thr Ile Leu Leu Gly Asp Arg Asn Leu Thr Ile Asp Glu Val Val Ser
            20                  25                  30

Val Ala Arg His Gly Ala Lys Val Asn Ile Ser Thr Ala Asp Asn Val
        35                  40                  45

Ala Gln Arg Ile Gln Ala Ser Cys Asp Tyr Ile Ala Glu Ala Val Ala
    50                  55                  60

Thr Gly Arg Pro Ile Tyr Gly Val Thr Ser Gly Phe Gly Gly Met Ala
65                  70                  75                  80

Asn Val Val Ile Ser Arg Glu Tyr Ala Asp Leu Leu Gln His Asn Leu
                85                  90                  95

Val Trp Tyr His Lys Val Gly Ala Gly Arg Lys Leu Pro Leu Thr Asp
            100                 105                 110

Val Arg Ala Ala Met Leu Leu Arg Val Asn Ser His Leu His Gly Ala
        115                 120                 125

Ser Gly Ile Arg Arg Glu Ile Val Gln Arg Met Glu Met Phe Leu Asn
    130                 135                 140

Ala Arg Val Thr Pro His Val Pro Glu Tyr Gly Ser Ile Gly Ala Ser
145                 150                 155                 160

Gly Asp Leu Thr Pro Leu Ser Tyr Ile Thr Gly Ala Leu Ile Gly Leu
                165                 170                 175

Asp Asp Arg Tyr Lys Val Asp Phe Asp Gly Glu Glu Ile Asp Ala Ile
            180                 185                 190
```

```
Thr Ala Leu Glu Arg Leu Gly Leu Pro Gln Leu Gln Leu Gln Ala Lys
        195                 200                 205

Glu Gly Leu Ala Met Met Asn Gly Thr Ser Val Met Thr Gly Ile Ala
    210                 215                 220

Ala Asn Cys Val Tyr Asp Thr Arg Leu Leu Met Ala Leu Thr Met Gly
225                 230                 235                 240

Ala His Ala Leu Ile Leu Gln Gly Leu Asn Gly Thr Asn Gln Ser Phe
                245                 250                 255

His Pro Phe Ile His Lys Leu Lys Pro His Pro Gly Gln Lys Trp Ala
            260                 265                 270

Ala Ser Thr Met Leu Asp Leu Leu Ala Gly Ser Arg Leu Ile Arg Glu
        275                 280                 285

Glu Leu Asp Gly Thr His Glu Tyr Arg Gly Gln Ala Pro Ile Gln Asp
    290                 295                 300

Arg Tyr Ser Leu Arg Cys Leu Ala Gln Tyr Met Gly Pro Ile Val Asp
305                 310                 315                 320

Gly Val Ser Gln Val Ala Gln Gln Val Glu Ile Glu Met Asn Ser Ala
                325                 330                 335

Thr Asp Asn Pro Leu Ile Asp Val Glu Asn Gln Ala Ser Tyr His Gly
            340                 345                 350

Gly Asn Phe Leu Gly Gln Tyr Ile Gly Met Gly Met Asp His Leu Arg
        355                 360                 365

Tyr Tyr Ile Gly Met Met Ala Lys His Leu Asp Val Gln Ile Ala Tyr
    370                 375                 380
```

```
Leu Val Ala Pro Glu Phe Asn Asn Gly Leu Pro Ala Ser Leu Val Gly
385                 390                 395                 400

Asn Lys Glu Arg Ile Val Asn Met Gly Leu Lys Gly Leu Gln Ile Thr
                405                 410                 415

Gly Asn Ser Ile Met Pro Leu Leu Ser Phe Tyr Gly Asn Ser Ile Ala
            420                 425                 430

Asp Arg Tyr Pro Thr His Ala Glu Gln Tyr Asn Gln Asn Ile Asn Ser
        435                 440                 445

Gln Gly Phe Ala Ala Ala Asn Leu Thr Arg Asn Ala Val Glu Ile Phe
    450                 455                 460

Gln Gln Tyr Met Ala Ile Ala Leu Met Phe Gly Val Gln Ala Val Asp
465                 470                 475                 480

Leu Arg Thr Tyr Ala Tyr Ala Gly His Tyr Asp Ala Ser Glu Cys Leu
                485                 490                 495

Ser Pro Thr Thr Arg Arg Leu Tyr Gln Ala Val Arg Glu Val Val Gly
            500                 505                 510

Gln Pro Ser Ser Ala Thr Arg Pro Tyr Ile Trp Asp Asp Arg Glu Gln
        515                 520                 525

Pro Leu Asp Glu His Ile Ala Lys Ile Ala Ala Asp Ile Ala Ala Glu
    530                 535                 540

Gly Val Ile Val Ala Ala Val Lys Asp Leu Leu Thr Ser Leu Lys
545                 550                 555
```